



SEQUENCE LISTING

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RUP, BONITA
VELDMAN, GEERTRUIDA M.

<120> HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
OF TREATMENT THEREWITH

<130> 08702.0081-01000

<140> 09/627,896

<141> 2000-07-27

<160> 32

<170> PatentIn Ver. 2.1

<210> 1

<211> 405

<212> DNA

<213> Murine sp.

<220>

<221> CDS

<222> (1)..(405)

<223> Anti-B7-2 heavy chain

<400> 1

atg ggt tgg aac tgt atc atc ttc ttt ctg gtt aca aca gct aca ggt
48

Met Gly Trp Asn Cys Ile Ile Phe Phe Leu Val Thr Thr Ala Thr Gly
1 5 10 15

gtg cac tcc cag gtc cag ctg cag cag tct ggg cct gag ctg gtg agg
96

Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Arg
20 25 30

cct ggg gaa tca gtg aag att tcc tgc aag ggt tcc ggc tac aca ttc
144

Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe
35 40 45

act gat tat gct ata cag tgg gtg aag cag agt cat gca aag agt cta
192

Thr Asp Tyr Ala Ile Gln Trp Val Lys Gln Ser His Ala Lys Ser Leu
50 55 60

gag tgg att gga gtt att aat att tac tat gat aat aca aac tac aac
240

Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn
65 70 75 80

cag aag ttt aag ggc aag gcc aca atg act gta gac aaa tcc tcc agc
288

Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser
85 90 95

aca gcc tat atg gaa ctt gcc aga ttg aca tct gag gat tct gcc atc
336

Thr Ala Tyr Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile
100 105 110

tat tac tgt gca aga gcg gcc tgg tat atg gac tac tgg ggt caa gga
384

Tyr Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly
115 120 125

acc tca gtc acc gtc tcc tca
405

Thr Ser Val Thr Val Ser Ser
130 135

<210> 2

<211> 135

<212> PRT

<213> Murine sp.

<220>

<223> Anti-B7-2 heavy chain

<400> 2

Met	Gly	Trp	Asn	Cys	Ile	Ile	Phe	Phe	Leu	Val	Thr	Thr	Ala	Thr	Gly
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Val	His	Ser	Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Val	Arg
			20					25					30		
Pro	Gly	Glu	Ser	Val	Lys	Ile	Ser	Cys	Lys	Gly	Ser	Gly	Tyr	Thr	Phe
		35					40					45			
Thr	Asp	Tyr	Ala	Ile	Gln	Trp	Val	Lys	Gln	Ser	His	Ala	Lys	Ser	Leu
	50					55					60				
Glu	Trp	Ile	Gly	Val	Ile	Asn	Ile	Tyr	Tyr	Asp	Asn	Thr	Asn	Tyr	Asn
65					70					75				80	
Gln	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Met	Thr	Val	Asp	Lys	Ser	Ser	Ser
				85					90					95	
Thr	Ala	Tyr	Met	Glu	Leu	Ala	Arg	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Ile
			100					105					110		
Tyr	Tyr	Cys	Ala	Arg	Ala	Ala	Trp	Tyr	Met	Asp	Tyr	Trp	Gly	Gln	Gly
		115					120					125			
Thr	Ser	Val	Thr	Val	Ser	Ser									
	130					135									

<210> 3
 <211> 396
 <212> DNA
 <213> Murine sp.

<220>
 <221> CDS
 <222> (1)..(396)
 <223> Anti-B7-2 light chain

<400> 3
 atg gat tca cag gcc cag gtt ctt ata ttg ctg ctg cta tgg gta tct
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 Met Asp Ser Gln Ala Gln Val Leu Ile Leu Leu Leu Leu Trp Val Ser
 1 5 10 15

ggt acc tgt ggg gac att gtg ctg tca cag tct cca tcc tcc ctg gct
96

Gly Thr Cys Gly Asp Ile Val Leu Ser Gln Ser Pro Ser Ser Leu Ala
20 25 30

gtg tca gca gga gag aag gtc act atg agc tgc aaa tcc agt cag agt
144

Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser
35 40 45

ctg ctc aac agt aga acc cga gag aac tac ttg gct tgg tac cag cag
192

Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp Tyr Gln Gln
50 55 60

aaa cca ggg cag tct cct aaa ctg ctg atc tac tgg gca tcc act agg
240

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
65 70 75 80

gaa tct ggg gtc cct gat cgc ttc aca ggc agt gga tct ggg aca gat
288

Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
85 90 95

ttc act ctc acc atc agc agt gtg cag gct gaa gac ctg gca gtt tat
336

Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr
100 105 110

tac tgc acg caa tct tat aat ctt tac acg ttc gga ggg ggg acc aag
384

Tyr Cys Thr Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gly Gly Thr Lys
115 120 125

ctg gaa ata aaa

396

Leu Glu Ile Lys

130

<210> 4

<211> 132

<212> PRT

<213> Murine sp.

<220>

<223> Anti-B7-2 light chain

<400> 4

Met	Asp	Ser	Gln	Ala	Gln	Val	Leu	Ile	Leu	Leu	Leu	Leu	Trp	Val	Ser	
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Gly	Thr	Cys	Gly	Asp	Ile	Val	Leu	Ser	Gln	Ser	Pro	Ser	Ser	Leu	Ala	
			20					25					30			
Val	Ser	Ala	Gly	Glu	Lys	Val	Thr	Met	Ser	Cys	Lys	Ser	Ser	Gln	Ser	
		35					40					45				
Leu	Leu	Asn	Ser	Arg	Thr	Arg	Glu	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	
	50					55					60					
Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg	
	65					70				75					80	
Glu	Ser	Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly	Ser	Gly	Ser	Gly	Thr	Asp	
				85					90					95		
Phe	Thr	Leu	Thr	Ile	Ser	Ser	Val	Gln	Ala	Glu	Asp	Leu	Ala	Val	Tyr	
			100					105					110			
Tyr	Cys	Thr	Gln	Ser	Tyr	Asn	Leu	Tyr	Thr	Phe	Gly	Gly	Gly	Thr	Lys	
		115					120					125				
Leu	Glu	Ile	Lys													
	130															

<210> 5

<211> 405

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Humanized
murine anti-human B7-2 heavy chain

<220>

<221> CDS

<222> (1)..(405)

<400> 5

atg ggt tgg aac tgt atc atc ttc ttt ctg gtt acc aca gct aca ggt
48

Met Gly Trp Asn Cys Ile Ile Phe Phe Leu Val Thr Thr Ala Thr Gly
1 5 10 15

gtg cac tcc cag gtc cag ctg gtg cag tct ggg gct gag gtg aag aag
96

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

cct ggg agc tca gtg aag gtg tcc tgc aaa gct tcc ggc tac aca ttc
144

Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

act gat tat gct ata cag tgg gtg aga cag gct cct gga cag ggc ctc
192

Thr Asp Tyr Ala Ile Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

gag tgg att gga gtt att aat att tac tat gat aat aca aac tac aac
240

Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn
65 70 75 80

cag aag ttt aag ggc aag gcc aca atg act gta gac aag tcg acg agc
288

Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Thr Ser
85 90 95

aca gcc tat atg gaa ctt agt tct ttg aga tct gag gat acg gcc gtt
336

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

tat tac tgt gca aga gcg gcc tgg tat atg gac tac tgg ggt caa ggt
384

Tyr Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly
115 120 125

acc ctt gtc acc gtc tcc tca
405

Thr Leu Val Thr Val Ser Ser
130 135

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Humanized
murine anti-human B7-2 heavy chain

<400> 6

Met	Gly	Trp	Asn	Cys	Ile	Ile	Phe	Phe	Leu	Val	Thr	Thr	Ala	Thr	Gly
1				5					10					15	

Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys
			20					25					30		

Pro	Gly	Ser	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe
		35					40					45			

Thr	Asp	Tyr	Ala	Ile	Gln	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu
	50					55					60				

Glu	Trp	Ile	Gly	Val	Ile	Asn	Ile	Tyr	Tyr	Asp	Asn	Thr	Asn	Tyr	Asn
65					70					75					80

Gln	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Met	Thr	Val	Asp	Lys	Ser	Thr	Ser
				85					90					95	

Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val
			100					105					110		

Tyr	Tyr	Cys	Ala	Arg	Ala	Ala	Trp	Tyr	Met	Asp	Tyr	Trp	Gly	Gln	Gly
		115					120					125			

Thr	Leu	Val	Thr	Val	Ser	Ser
	130					135

<210> 7

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Humanized
murine anti-human B7-2 light chain

<220>

<221> CDS

<222> (1)..(396)

<400> 7

atg gat tca cag gcc cag gtt ctt ata ttg ctg ctg cta tgg gta tct

48

Met Asp Ser Gln Ala Gln Val Leu Ile Leu Leu Leu Leu Trp Val Ser

1

5

10

15

ggc acc tgt ggg gac att gtg ctg aca cag tct cca gat tcc ctg gct

96

Gly Thr Cys Gly Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala

20

25

30

gta agc tta gga gag agg gcc act att agc tgc aaa tcc agt cag agt

144

Val Ser Leu Gly Glu Arg Ala Thr Ile Ser Cys Lys Ser Ser Gln Ser

35

40

45

ctg ctc aac agt aga acc cga gag aac tac ttg gct tgg tac cag cag

192

Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp Tyr Gln Gln

50

55

60

aaa cca ggg cag cct cct aaa ctg ctg atc tac tgg gca tcc act agg

240

Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg

65

70

75

80

gaa tct ggg gtc cct gat cgc ttc agt ggc agt gga tct ggg aca gat

288

Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp

85

90

95

ttc act ctc acc atc agc agt ctg cag gct gaa gac gtg gca gtt tat

336

Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr

100

105

110

tac tgc acg caa tct tat aat ctt tac acg ttc gga cag ggg acc aag

384

Tyr Cys Thr Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gln Gly Thr Lys

115

120

125

gtg gaa ata aaa
396
Val Glu Ile Lys
130

<210> 8
<211> 132
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Humanized
murine anti-human B7-2 light chain

<400> 8
Met Asp Ser Gln Ala Gln Val Leu Ile Leu Leu Leu Leu Trp Val Ser
1 5 10 15
Gly Thr Cys Gly Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala
20 25 30
Val Ser Leu Gly Glu Arg Ala Thr Ile Ser Cys Lys Ser Ser Gln Ser
35 40 45
Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp Tyr Gln Gln
50 55 60
Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
65 70 75 80
Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
85 90 95
Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
100 105 110
Tyr Cys Thr Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gln Gly Thr Lys
115 120 125
Val Glu Ile Lys
130

<210> 9
<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CDR1 of
humanized murine anti-human B7-2 heavy chain

<220>

<221> CDS

<222> (1)..(15)

<400> 9

gat tat gct ata cag

15

Asp Tyr Ala Ile Gln

1

5

<210> 10

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CDR1 of humanized
murine anti-human B7-2 heavy chain

<400> 10

Asp Tyr Ala Ile Gln

1

5

<210> 11

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CDR2 of
humanized murine anti-human B7-2 heavy chain

<220>

<221> CDS

<222> (1)..(51)

<400> 11

gtt att aat att tac tat gat aat aca aac tac aac cag aag ttt aag
48

Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn Gln Lys Phe Lys
1 5 10 15

ggc
51
Gly

<210> 12
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CDR2 of humanized
murine anti-human B7-2 heavy chain

<400> 12
Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn Gln Lys Phe Lys
1 5 10 15

Gly

<210> 13
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CDR3 of
humanized murine anti-human B7-2 heavy chain

<220>
<221> CDS
<222> (1)..(21)

<400> 13
gcg gcc tgg tat atg gac tac
21
Ala Ala Trp Tyr Met Asp Tyr
1 5

<210> 14

<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CDR3 of humanized
murine anti-human B7-2 heavy chain

<400> 14
Ala Ala Trp Tyr Met Asp Tyr
1 5

<210> 15
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CDR1 of
humanized murine anti-human B7-2 light chain

<220>
<221> CDS
<222> (1)..(51)

<400> 15
aaa tcc agt cag agt ctg ctc aac agt aga acc cga gag aac tac ttg
48
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu
1 5 10 15

gct
51
Ala

<210> 16
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CDR1 of humanized
murine anti-human B7-2 light chain

<400> 16

Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu
1 5 10 15

Ala

<210> 17

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CDR2 of
humanized murine anti-human B7-2 light chain

<220>

<221> CDS

<222> (1)..(21)

<400> 17

tgg gca tcc act agg gaa tct
21

Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 18

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CDR2 of humanized
murine anti-human B7-2 light chain

<400> 18

Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 19

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CDR3 of

humanized murine anti-human B7-2 light chain

<220>

<221> CDS

<222> (1)..(24)

<400> 19

acg caa tct tat aat ctt tac acg

24

Thr Gln Ser Tyr Asn Leu Tyr Thr

1

5

<210> 20

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CDR3 of humanized
murine anti-human B7-2 light chain

<400> 20

Thr Gln Ser Tyr Asn Leu Tyr Thr

1

5

<210> 21

<211> 1960

<212> DNA

<213> Mus sp.

<220>

<221> CDS

<222> (12)..(408)

<220>

<221> CDS

<222> (768)..(1087)

<223> 3D1 light chain

<400> 21

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50

Met Asp Ser Gln Ala Gln Val Leu Ile Leu Leu Leu Leu

1

5

10

tgg gta tct ggc acc tgt ggg gac att gtg ctg aca cag tct cca gat
98

Trp Val Ser Gly Thr Cys Gly Asp Ile Val Leu Thr Gln Ser Pro Asp
15 20 25

tcc ctg gct gta agc tta gga gag agg gcc act att agc tgc aaa tcc
146

Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Ser Cys Lys Ser
30 35 40 45

agt cag agt ctg ctc aac agt aga acc cga gag aac tac ttg gct tgg
194

Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp
50 55 60

tac cag cag aaa cca ggg cag cct cct aaa ctg ctg atc tac tgg gca
242

Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala
65 70 75

tcc act agg gaa tct ggg gtc cct gat cgc ttc agt ggc agt gga tct
290

Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser
80 85 90

ggg aca gat ttc act ctc acc atc agc agt ctg cag gct gaa gac gtg
338

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val
95 100 105

gca gtt tat tac tgc agc caa tct tat aat ctt tac acg ttc gga cag
386

Ala Val Tyr Tyr Cys Ser Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gln
110 115 120 125

ggg acc aag gtg gaa ata aaa c gtaagtagtc ttctcaactc tagaaattct
438

Gly Thr Lys Val Glu Ile Lys
130

aaactctgag ggggtcggat gacgtggcca ttctttgcct aaagcattga gtttactgca
498

aggtcagaaa agcatgcaaaa gccctcagaa tggctgcaaa gagctccaac aaaacaattt
558

agaactttat taaggaatag ggggaagcta ggaagaaact caaaacatca agatttttaa
618

tacgcttctt ggtctccttg ctataattat ctgggataag catgctgttt tctgtctgtc
678

cctaacatgc cctgtgatta tccgcaaaca acacacccaa gggcagaact ttgttactta
738

aacaccatcc tgtttgcttc tttcctcag ga act gtg gct gca cca tct gtc
790

Arg Thr Val Ala Ala Pro Ser Val
135 140

ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga act gcc tct
838

Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser
145 150 155

gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta cag
886

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln
160 165 170

tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc
934

Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val
175 180 185

aca gag cag gac agc aag gac agc acc tac agc ctc agc agc acc ctg
982

Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu
190 195 200

acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa
1030

Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu
205 210 215 220

gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg
1078

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg
225 230 235

gga gag tgt tagagggaga agtgcccca cctgctcctc agttccagcc
1127

Gly Glu Cys

tgacccctc ccacctttg gcctctgacc cttttccac aggggaccta cccctattgc
1187

ggctctccag ctcatctttc acctcaccce cctcctctc cttggcttta attatgctaa
1247

tgttggagga gaatgaataa ataaagtga tctttgcacc tgtggtttct ctctttctc
1307

atttaataat tattatctgt tgttttacca actactcaat ttctcttata agggactaaa
1367

tatgtagtca tcctaaggcg cataaccatt tataaaaatc atccttcatt ctattttacc
1427

ctatcatcct ctgcaagaca gtcctccctc aaaccacaa gccttctgtc ctcacagtcc
1487

cctgggccat ggtaggagag acttgcttcc ttgttttccc ctctcagca agccctcata
1547

gtccttttta agggtgacag gtcttacagt catatatcct ttgattcaat tccctgggaa
1607

tcaaccaaag caaatttttc aaaagaagaa acctgctata aagagaatca ttcattgcaa
1667

catgatataa aataacaaca caataaaagc aattaaataa acaaacaata gggaaatgtt
1727

taagttcatc atggtactta gacttaatgg aatgtcatgc cttatttaca tttttaaaca
1787

ggtactgagg gactcctgtc tgccaagggc cgtattgagt actttccaca acctaattha
1847

atccacacta tactgtgaga ttaaaaacat tcattaaaat gttgcaaagg ttctataaag
1907

ctgagagaca aatatattct ataactcagc aatcccactt ctaggatcaa ttc
1960

<210> 22

<211> 239

<212> PRT

<213> Mus sp.

<223> 3D1 light chain

<400> 22

Met	Asp	Ser	Gln	Ala	Gln	Val	Leu	Ile	Leu	Leu	Leu	Leu	Trp	Val	Ser
1				5					10					15	

Gly	Thr	Cys	Gly	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Asp	Ser	Leu	Ala
			20					25					30		

Val	Ser	Leu	Gly	Glu	Arg	Ala	Thr	Ile	Ser	Cys	Lys	Ser	Ser	Gln	Ser
		35					40					45			

Leu	Leu	Asn	Ser	Arg	Thr	Arg	Glu	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln
	50					55					60				

Lys	Pro	Gly	Gln	Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg
65					70					75					80

Glu	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp
				85					90					95	

Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Ala	Glu	Asp	Val	Ala	Val	Tyr
		100						105					110		

Tyr	Cys	Ser	Gln	Ser	Tyr	Asn	Leu	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys
		115					120					125			

Val	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro
	130					135					140				

Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu
145					150					155					160

Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp
			165						170					175	

Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp
		180						185					190		

Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys
		195					200					205			

Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln
	210					215					220				

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230 235

<210> 23
 <211> 2249
 <212> DNA
 <213> 3D1 heavy chain

<220>
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 <222> (12)..(417)

<220>
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 <222> (655)..(948)

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 <222> (1341)..(1376)

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 <222> (1495)..(1821)

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 <222> (1919)..(2238)

<400> 23
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 50

Met Gly Trp Asn Cys Ile Ile Phe Phe Leu Val Thr Thr
 1 5 10

gct aca ggt gtg cac tcc cag gtc cag ctg gtg cag tct ggg gct gag
 98

Ala Thr Gly Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu
 15 20 25

gtg aag aag cct ggg agc tca gtg aag gtg tcc tgc aaa gct tcc ggc
 146

Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly
 30 35 40 45

tac aca ttc act gat tat gct ata cag tgg gtg aga cag gct cct gga
194

Tyr Thr Phe Thr Asp Tyr Ala Ile Gln Trp Val Arg Gln Ala Pro Gly
50 55 60

cag ggc ctc gag tgg att gga gtt att aat att tac tat gat aat aca
242

Gln Gly Leu Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr
65 70 75

aac tac aac cag aag ttt aag ggc aag gcc aca atg act gta gac aag
290

Asn Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys
80 85 90

tcg acg agc aca gcc tat atg gaa ctt agt tct ttg aga tct gag gat
338

Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp
95 100 105

acg gcc gtt tat tac tgt gca aga gcg gcc tgg tat atg gac tac tgg
386

Thr Ala Val Tyr Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp
110 115 120 125

ggc caa ggt acc ctt gtc acc gtc tcc tca g gtgagtcctt aaaacctcta
437

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
130 135

gagctttctg gggcgagccg ggccctgactt tggctttggg gcagggagtg ggctaagggtg
497

aggcaggtgg cgccagccag gtgcacaccc aatgcccgtg agcccagaca ctggaccctg
557

cctggaccct cgtggataga caagaaccga ggggcctctg cgccctgggc ccagctctgt
617

cccacaccgc ggtcacatgg caccacctct cttgcag cc tcc acc aag ggc cca
671

Ala Ser Thr Lys Gly Pro
140

tgc gtc ttc ccc ctg gcg ccc tgc tcc agg agc acc tcc gag agc aca
719

Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr
145 150 155

gcg gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg
767

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
160 165 170

gtg tgc tgg aac tca ggc gct ctg acc agc ggc gtg cac acc ttc cca
815

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
175 180 185

gct gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc
863

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
190 195 200 205

gtg ccc tcc agc aac ttc ggc acc cag acc tac acc tgc aac gta gat
911

Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp
210 215 220

cac aag ccc agc aac acc aag gtg gac aag aca gtt g gtgagaggcc
958

His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val
225 230

agctcagggga gggaggggtgt ctgctggaag ccaggctcag ccctcctgcc tggacgcacc
1018

ccggctgtgc agccccagcc cagggcagca aggcaggccc catctgtctc ctcacccgga
1078

ggcctctgcc cgccccactc atgctcaggg agaggggtctt ctggcttttt ccaccaggct
1138

ccaggcaggc acaggctggg tgcccctacc ccaggccctt cacacacagg ggcagggtgct
1198

tggtcagac ctgccaaaag ccatatccgg gaggaccctg ccctgacct aagccgaccc
1258

caaaggccaa actgtccact ccctcagctc ggacaccttc tctcctccca gatccgagta
1318

actcccaatc ttctctctgc ag ag cgc aaa tgt tgt gtc gag tgc cca ccg
1369

Glu Arg Lys Cys Cys Val Glu Cys Pro Pro
235 240

tgc cca g gtaagccagc ccaggcctcg ccctccagct caaggcggga caggtgccct
1426

Cys Pro
245

agagtagcct gcatccaggg acaggcccca gctgggtgct gacacgtcca cctccatctc
1486

ttcctcag ca cca cct gcg gca gca ccg tca gtc ttc ctc ttc ccc cca
1535

Ala Pro Pro Ala Ala Ala Pro Ser Val Phe Leu Phe Pro Pro
250 255

aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc acg tgc
1583

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
260 265 270 275

gtg gtg gtg gac gtg agc cac gaa gac ccc gag gtc cag ttc aac tgg
1631

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp
280 285 290

tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag cca cgg gag
1679

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
295 300 305

gag cag ttc aac agc acg ttc cgt gtg gtc agc gtc ctc acc gtt gtg
1727

Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val
310 315 320

cac cag gac tgg ctg aac ggc aag gag tac aag tgc aag gtc tcc aac
1775

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
325 330 335

aaa ggc ctc cca gcc ccc atc gag aaa acc atc tcc aaa acc aaa g
1821

Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys
340 345 350

gtgggacccg cgggggtatga gggccacatg gacagaggcc ggctcggccc accctctgcc
1881

ctgggagtga cgcctgtgcc aacctctgtc cctacag gg cag ccc cga gaa cca
1935

Gly Gln Pro Arg Glu Pro
355 360

cag gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag
1983

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
365 370 375

gtc agc ctg acc tgc ctg gtc aaa ggc ttc tac ccc agc gac atc gcc
2031

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
380 385 390

gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc aca
2079

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
395 400 405

cct ccc atg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc
2127

Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
410 415 420

acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc
2175

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
425 430 435 440

gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc
2223

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
445 450 455

ctg tcc ccg ggt aaa tgagtgaatt c

2249

Leu Ser Pro Gly Lys

460

<210> 24

<211> 462

<212> PRT

<213> 3D1 heavy chain

<400> 24

Met Gly Trp Asn Cys Ile Ile Phe Phe Leu Val Thr Thr Ala Thr Gly
1 5 10 15

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Thr Asp Tyr Ala Ile Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn
65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Thr Ser
85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly
115 120 125

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
130 135 140

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
145 150 155 160

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
165 170 175

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
180 185 190

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
195 200 205

Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro
210 215 220

Ser Asn Thr Lys Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val
225 230 235 240

Glu Cys Pro Pro Cys Pro Ala Pro Pro Ala Ala Ala Pro Ser Val Phe
245 250 255

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
260 265 270

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
275 280 285

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
290 295 300

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val
305 310 315 320

Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
325 330 335

Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
340 345 350

Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
355 360 365

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
370 375 380

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
385 390 395 400

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp
405 410 415

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
420 425 430

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
435 440 445

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455 460

<210> 25

<211> 327

<212> DNA

<213> Homo sapiens

<223> III2R light chain variable region

<400> 25

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc
60

atcacttgcc gggcgagtca gggcattagc aattatttag cctgggtatca gcagaaacca
120

gggaaagtgc ctaagctcct gatctatgct gcatccactt tgcaatcagg ggtcccatct
180

cggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct
240

gaagatgttg caacttatta ctgtcaaaag tataacagtg cccctccgag tacgttcggc
300

caagggacca aggtggaaat caaacgt
327

<210> 26
<211> 339
<212> DNA
<213> Homo sapiens
<223> H2F light chain variable region

<400> 26
gacatccagt tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc
60

atcaactgca agtccagcca gagtgtttta tacagctcca acaacaagaa ttacttaact
120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctaccgg
180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc
240

atcagcagcc tgcaggctga agatgtggca gtttattact gtcagcaata ttatagtact
300

cctcgaacgt tcggccaagg gaccaaggtg gaaatcaaa
339

<210> 27
<211> 95
<212> PRT
<213> Homo sapiens
<223> III2R light chain variable region

<400> 27

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Lys Tyr Asn Ser Ala Pro
85 90 95

<210> 28
<211> 101
<212> PRT
<213> Homo sapiens
<223> H2F light chain variable region

<400> 28

Asp Ile Gln Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

Ser Asn Asn Lys Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln Pro
35 40 45

Pro Lys Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Thr Pro

<210> 29
<211> 368
<212> DNA
<213> Homo sapiens
<223> III2R heavy chain variable region

<400> 29
agggtgcagct ggtgcagtct ggggctgagg tgaagaagcc tgggtcctcg gtaaaggctt
60

cctgcaaggc ttctggaggc accttcagta gttatactat cagctgggtg cgacaggccc
120

ctggacaagg gcttgagtgg atgggaagga tcatgcctat ccttggacta gcaaattacg
180

cacagaagtt ccagggcaga gtcacgatta ccgcggacaa atccacgagc acagcctaca
240

tggagctgag cagcctgaga tctgaggaca cggccgtgta ttactgtgcg agagatccccg
300

attatgtttg ggggagcgac aactgggtcg acccctgggg ccaggggaacc ctgctcatcg
360

tctcctca
368

<210> 30
<211> 358
<212> DNA
<213> Homo sapiens
<223> H2F heavy chain variable region

<400> 30
gtgcagctgg tggagtctgg gggaggcttg gtcaagcctg gagggtcctt gagactctcc
60

tgtgcagcct cggattcacc ttactagga atcctacgag ctgggtacgc caggctccag
120

ggaaggggct ggagtgggtg gttaatatataa tggtagtcgg aattgaacca tactatgcgg
180

actctgtgaa gggccgattc accatctcca gaggcaacgc caagaactca ctgtatctgc
240

aatgaacag cctgagagcc gaggacacgg ccgtgtatta ctgtgcgaga gggatctgtc
300

ttatgacaga ggctactttg actactgggg ccagggaacc ctggtcaccg tctcctca
358

<210> 31
<211> 97
<212> PRT
<213> Homo sapiens
<223> III2R heavy chain variable region

<400> 31

Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ser	Ser
1				5					10					15	

Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Gly	Thr	Phe	Ser	Ser	Tyr	Thr
			20					25					30		

Ile	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	Gly
		35					40					45			

Arg	Ile	Met	Pro	Ile	Leu	Gly	Leu	Ala	Asn	Tyr	Ala	Gln	Lys	Phe	Gln
	50					55					60				

Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Lys	Ser	Thr	Ser	Thr	Ala	Tyr	Met
65					70					75				80	

Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala
				85					90					95	

Arg

<210> 32
<211> 98
<212> PRT
<213> Homo sapiens
<223> H2F heavy chain variable region

<400> 32

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser
1 5 10 15

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr Tyr
20 25 30

Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
35 40 45

Tyr Ile Ser Ser Arg Gly Ser Glu Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg
